03 60

OIPE

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ENTERED

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 3 <110> APPLICANT: STRITTMATTER, STEPHEN M.
 4         CATE, RICHARD L.
 5         SAH, DINAH W.Y.
 7 <120> TITLE OF INVENTION: NOGO RECEPTOR HOMOLOGS
 9 <130> FILE REFERENCE: A116US
11 <140> CURRENT APPLICATION NUMBER: 09/972,546
12 <141> CURRENT FILING DATE: 2001-10-06
14 <150> PRIOR APPLICATION NUMBER: 60/238,361
15 <151> PRIOR FILING DATE: 2000-10-06
17 <160> NUMBER OF SEQ ID NOS: 19
19 <170> SOFTWARE: PatentIn Ver. 2.1
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22 <211> LENGTH: 1260
23 <212> TYPE: DNA
24 <213> ORGANISM: Homo sapiens
26 <400> SEQUENCE: 1
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29 ccgcccaccg tgagctgcca ggccaacaac ttctcctctg tgccgctgtc cctgccaccc 180
30 agcactcagc gactcttcct gcagaacaac ctcatccgca cgctgcggcc aggcaccttt 240
31 gggtccaacc tgctcaccct gtggctcttc tccaacaacc tctccaccat ctacccgggc 300
32 actttccgcc acttgcaagc cctggaggag ctggacctcg gtgacaaccg gcacctgcgc 360
33 tcgctggagc ccgacacctt ccagggcctg gagcggctgc agtcgctgca tttgtaccgc 420
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36 ctgagccacc tcttcctcca cgggaaccgc ctgcggctgc tcacagagca cgtgtttcgc 600
37 ggcctgggca gcctggaccg gctgctgctg cacgggaacc ggctgcaggg cgtgcaccgc 660
38 gcggccttcc gcggcctcag ccgcctcacc atcctctacc tgttcaacaa cagcctggcc 720
39 tcgctgcccg gcgaggcgct cgccgacctg ccctcgctcg agttcctgcg gctcaacgct 780
40 aacccctggg cgtgcgactg ccgcgcgcgg ccgctctggg cctggttcca gcgcgcgcgc 840
41 gtgtccagct ccgacgtgac ctgcgccacc ccccggagc gccagggccg agacctgcgc 900
42 gcgctccgcg aggccgactt ccaggcgtgt ccgcccgcgg cacccacgcg gccgggcagc 960
43 cgcgcccgcg gcaacagctc ctccaaccac ctgtacgggg tggccgaggc cggggcgccag 1020
44 ccagccgatc cctccaccct ctaccgagat ctgcctgccg aagactcgcg ggggcgccag 1080
45 ggcggggacg cgcctactga ggacgactac tggggggggct acggggtga ggaccagcga 1140
46 ggggagcaga tgtgcccccgg cgctgcctgc caggcgcccc cggactcccg aggccctgcg 1200
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52 <212> TYPE: PRT
53 <213> ORGANISM: Homo sapiens
55 <400> SEQUENCE: 2
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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/972,546

DATE: 02/08/2002
TIME: 12:07:16

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Output Set: N:\CRF3\02082002\I972546.raw

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63          35                  40                  45
65  Asn Asn Phe Ser Ser Val Pro Leu Ser Leu Pro Pro Ser Thr Gln Arg
66      50                  55                  60
68  Leu Phe Leu Gln Asn Asn Leu Ile Arg Thr Leu Arg Pro Gly Thr Phe
69  65                  70                  75                  80
71  Gly Ser Asn Leu Leu Thr Leu Trp Leu Phe Ser Asn Asn Leu Ser Thr
72              85                  90                  95
74  Ile Tyr Pro Gly Thr Phe Arg His Leu Gln Ala Leu Glu Glu Leu Asp
75              100                 105                 110
77  Leu Gly Asp Asn Arg His Leu Arg Ser Leu Glu Pro Asp Thr Phe Gln
78      115                 120                 125
80  Gly Leu Glu Arg Leu Gln Ser Leu His Leu Tyr Arg Cys Gln Leu Ser
81      130                 135                 140
83  Ser Leu Pro Gly Asn Ile Phe Arg Gly Leu Val Ser Leu Gln Tyr Leu
84  145                 150                 155                 160
86  Tyr Leu Gln Glu Asn Ser Leu Leu His Leu Gln Asp Asp Leu Phe Ala
87              165                 170                 175
89  Asp Leu Ala Asn Leu Ser His Leu Phe Leu His Gly Asn Arg Leu Arg
90              180                 185                 190
92  Leu Leu Thr Glu His Val Phe Arg Gly Leu Gly Ser Leu Asp Arg Leu
93      195                 200                 205
95  Leu Leu His Gly Asn Arg Leu Gln Gly Val His Arg Ala Ala Phe Arg
96      210                 215                 220
98  Gly Leu Ser Arg Leu Thr Ile Leu Tyr Leu Phe Asn Asn Ser Leu Ala
99  225                 230                 235                 240
101 Ser Leu Pro Gly Glu Ala Leu Ala Asp Leu Pro Ser Leu Glu Phe Leu
102                 245                 250                 255
104 Arg Leu Asn Ala Asn Pro Trp Ala Cys Asp Cys Arg Ala Arg Pro Leu
105                 260                 265                 270
107 Trp Ala Trp Phe Gln Arg Ala Arg Val Ser Ser Ser Asp Val Thr Cys
108         275                 280                 285
110 Ala Thr Pro Pro Glu Arg Gln Gly Arg Asp Leu Arg Ala Leu Arg Glu
111     290                 295                 300
113 Ala Asp Phe Gln Ala Cys Pro Pro Ala Ala Pro Thr Arg Pro Gly Ser
114 305                 310                 315                 320
116 Arg Ala Arg Gly Asn Ser Ser Ser Asn His Leu Tyr Gly Val Ala Glu
117                 325                 330                 335
119 Ala Gly Ala Pro Pro Ala Asp Pro Ser Thr Leu Tyr Arg Asp Leu Pro
120             340                 345                 350
122 Ala Glu Asp Ser Arg Gly Arg Gln Gly Gly Asp Ala Pro Thr Glu Asp
123     355                 360                 365
125 Asp Tyr Trp Gly Gly Tyr Gly Gly Glu Asp Gln Arg Gly Glu Gln Met
126   370                 375                 380
128 Cys Pro Gly Ala Ala Cys Gln Ala Pro Pro Asp Ser Arg Gly Pro Ala
129 385                 390                 395                 400
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134 Pro His His Leu
135             420
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139 <211> LENGTH: 1383
140 <212> TYPE: DNA
141 <213> ORGANISM: Mus sp.
143 <400> SEQUENCE: 3
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146 tgtcctcgag actgtgtgtg ctaccctgcg cccatgactg tcagctgcca ggcacacaac 180
147 tttgctgcca tcccggaggg gggccacttc agccccgcca tggtcaccct ctggatctac 240
148 cgcatcacct tcctccagca gggccacttc agccccgcca tggtcaccct ctggatctac 300
149 tccaacaaca tcactttcat tgctcccaac accttcgagg gctttgtgca tctggaggag 360
150 ctagaccttg gagacaaccg acagctgcga acgctggcac ccgagacctt ccaaggcctg 420
151 gtgaagcttc acgccctcta cctctataag tgtggactga gcgccctgcc cgcaggcatc 480
152 tttggtggcc tgcacagcct gcagtatctc tacttgcagg acaaccatat cgagtacctc 540
153 caagatgaca tctttgtgga cctggtcaat ctcagtcact tgtttctcca tggtaacaag 600
154 ctatggagcc tgggccaagg catcttccgg ggcctggtga acctggaccg gttgctgctg 660
155 catgagaacc agctacagtg ggttcaccac aaggctttcc atgacctcca caggctaacc 720
156 accctctttc tcttcaacaa cagcctcact gagctgcagg gtgactgtct ggcccccctg 780
157 gtggccttgg agttccttcg cctcaatggg aatgcttggg actgtggctg ccgggcacgt 840
158 tccctgtggg aatggctgcg aaggttccgt ggctctagct ctgctgtccc ctgcgcgacc 900
159 cccgagctgc ggcaaggcca ggatctgaag ctgctgaggg tggaggactt ccggaactgc 960
160 acaggaccag tgtctcctca ccagatcaag tctcacacgc ttaccacctc tgacagggct 1020
161 gcccgcaagg agcaccatcc gtcccatggg gcctccaggg acaaaggcca cccacatggc 1080
162 catccgcctg gctccaggtc aggttacaag aaggcaggca agaactgcac cagccacagg 1140
163 aaccggaacc agatctctaa ggtgagctct gggaaagagc ttaccgaact gcaggactat 1200
164 gcccccgact atcagcacaa gttcagcttt gacatcatgc ccaccgcacg acccaagagg 1260
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171 <211> LENGTH: 461
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180             20             25             30
182 Gly Glu Leu Pro Leu Gly Gly Gly Cys Pro Arg Asp Cys Val Cys Tyr
183             35             40             45
185 Pro Ala Pro Met Thr Val Ser Cys Gln Ala His Asn Phe Ala Ala Ile
186             50             55             60
188 Pro Glu Gly Ile Pro Glu Asp Ser Glu Arg Ile Phe Leu Gln Asn Asn
189 65             70             75             80
191 Arg Ile Thr Phe Leu Gln Gln Gly His Phe Ser Pro Ala Met Val Thr
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192                  85                  90                  95
194 Leu Trp Ile Tyr Ser Asn Asn Ile Thr Phe Ile Ala Pro Asn Thr Phe
195             100                 105                 110
197 Glu Gly Phe Val His Leu Glu Glu Leu Asp Leu Gly Asp Asn Arg Gln
198         115                 120                 125
200 Leu Arg Thr Leu Ala Pro Glu Thr Phe Gln Gly Leu Val Lys Leu His
201     130                 135                 140
203 Ala Leu Tyr Leu Tyr Lys Cys Gly Leu Ser Ala Leu Pro Ala Gly Ile
204 145                 150                 155                 160
206 Phe Gly Gly Leu His Ser Leu Gln Tyr Leu Tyr Leu Gln Asp Asn His
207             165                 170                 175
209 Ile Glu Tyr Leu Gln Asp Asp Ile Phe Val Asp Leu Val Asn Leu Ser
210         180                 185                 190
212 His Leu Phe Leu His Gly Asn Lys Leu Trp Ser Leu Gly Gln Gly Ile
213         195                 200                 205
215 Phe Arg Gly Leu Val Asn Leu Asp Arg Leu Leu Leu His Glu Asn Gln
216     210                 215                 220
218 Leu Gln Trp Val His His Lys Ala Phe His Asp Leu His Arg Leu Thr
219 225                 230                 235                 240
221 Thr Leu Phe Leu Phe Asn Asn Ser Leu Thr Glu Leu Gln Gly Asp Cys
222             245                 250                 255
224 Leu Ala Pro Leu Val Ala Leu Glu Phe Leu Arg Leu Asn Gly Asn Ala
225         260                 265                 270
227 Trp Asp Cys Gly Cys Arg Ala Arg Ser Leu Trp Glu Trp Leu Arg Arg
228         275                 280                 285
230 Phe Arg Gly Ser Ser Ser Ala Val Pro Cys Ala Thr Pro Glu Leu Arg
231     290                 295                 300
233 Gln Gly Gln Asp Leu Lys Leu Leu Arg Val Glu Asp Phe Arg Asn Cys
234 305                 310                 315                 320
236 Thr Gly Pro Val Ser Pro His Gln Ile Lys Ser His Thr Leu Thr Thr
237             325                 330                 335
239 Ser Asp Arg Ala Ala Arg Lys Glu His His Pro Ser His Gly Ala Ser
240         340                 345                 350
242 Arg Asp Lys Gly His Pro His Gly His Pro Pro Gly Ser Arg Ser Gly
243         355                 360                 365
245 Tyr Lys Lys Ala Gly Lys Asn Cys Thr Ser His Arg Asn Arg Asn Gln
246     370                 375                 380
248 Ile Ser Lys Val Ser Ser Gly Lys Glu Leu Thr Glu Leu Gln Asp Tyr
249 385                 390                 395                 400
251 Ala Pro Asp Tyr Gln His Lys Phe Ser Phe Asp Ile Met Pro Thr Ala
252             405                 410                 415
254 Arg Pro Lys Arg Lys Gly Lys Cys Ala Arg Arg Thr Pro Ile Arg Ala
255         420                 425                 430
257 Pro Ser Gly Val Gln Gln Ala Ser Ser Gly Thr Ala Leu Gly Ala Pro
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261     450                 455                 460
264 <210> SEQ ID NO: 5
265 <211> LENGTH: 473
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RAW SEQUENCE LISTING   DATE: 02/08/2002
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Input Set : A:\A116us.app
Output Set: N:\CRF3\02082002\I972546.raw

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267 <213> ORGANISM: Homo sapiens
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273 Trp Leu Gln Ala Trp Gln Val Ala Ala Pro Cys Pro Gly Ala Cys Val
274              20                  25                  30
276 Cys Tyr Asn Glu Pro Lys Val Thr Thr Ser Cys Pro Gln Gln Gly Leu
277          35                  40                  45
279 Gln Ala Val Pro Val Gly Ile Pro Ala Ala Ser Gln Arg Ile Phe Leu
280      50                  55                  60
282 His Gly Asn Arg Ile Ser His Val Pro Ala Ala Ser Phe Arg Ala Cys
283 65                  70                  75                  80
285 Arg Asn Leu Thr Ile Leu Trp Leu His Ser Asn Val Leu Ala Arg Ile
286              85                  90                  95
288 Asp Ala Ala Ala Phe Thr Gly Leu Ala Leu Leu Glu Gln Leu Asp Leu
289          100                 105                 110
291 Ser Asp Asn Ala Gln Leu Arg Ser Val Asp Pro Ala Thr Phe His Gly
292          115                 120                 125
294 Leu Gly Arg Leu His Thr Leu His Leu Asp Arg Cys Gly Leu Gln Glu
295      130                 135                 140
297 Leu Gly Pro Gly Leu Phe Arg Gly Leu Ala Ala Leu Gln Tyr Leu Tyr
298 145                 150                 155                 160
300 Leu Gln Asp Asn Ala Leu Gln Ala Leu Pro Asp Asp Thr Phe Arg Asp
301              165                 170                 175
303 Leu Gly Asn Leu Thr His Leu Phe Leu His Gly Asn Arg Ile Ser Ser
304              180                 185                 190
306 Val Pro Glu Arg Ala Phe Arg Gly Leu His Ser Leu Asp Arg Leu Leu
307      195                 200                 205
309 Leu His Gln Asn Arg Val Ala His Val His Pro His Ala Phe Arg Asp
310      210                 215                 220
312 Leu Gly Arg Leu Met Thr Leu Tyr Leu Phe Ala Asn Asn Leu Ser Ala
313 225                 230                 235                 240
315 Leu Pro Thr Glu Ala Leu Ala Pro Leu Arg Ala Leu Gln Tyr Leu Arg
316              245                 250                 255
318 Leu Asn Asp Asn Pro Trp Val Cys Asp Cys Arg Ala Arg Pro Leu Trp
319              260                 265                 270
321 Ala Trp Leu Gln Lys Phe Arg Gly Ser Ser Ser Glu Val Pro Cys Ser
322      275                 280                 285
324 Leu Pro Gln Arg Leu Ala Gly Arg Asp Leu Lys Arg Leu Ala Ala Asn
325      290                 295                 300
327 Asp Leu Gln Gly Cys Ala Val Ala Thr Gly Pro Tyr His Pro Ile Trp
328 305                 310                 315                 320
330 Thr Gly Arg Ala Thr Asp Glu Glu Pro Leu Gly Leu Pro Lys Cys Cys
331              325                 330                 335
333 Gln Pro Asp Ala Ala Asp Lys Ala Ser Val Leu Glu Pro Gly Arg Pro
334              340                 345                 350
336 Ala Ser Ala Gly Asn Ala Leu Lys Gly Arg Val Pro Pro Gly Asp Ser
337          355                 360                 365
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Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding
explanation is presented in the <220> to <223> fields of
each sequence using n or Xaa.

VERIFICATION SUMMARY   DATE: 02/08/2002
PATENT APPLICATION: US/09/972,546   TIME: 12:07:17

Input Set : A:\All6us.app
Output Set: N:\CRF3\02082002\I972546.raw

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L:775  M:341 W:  (46) "n" or "Xaa" used, for SEQ ID#:6
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L:781  M:341 W:  (46) "n" or "Xaa" used, for SEQ ID#:6
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L:796  M:341 W:  (46) "n" or "Xaa" used, for SEQ ID#:6
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L:1178 M:341 W:  (46) "n" or "Xaa" used, for SEQ ID#:11
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L:1430 M:341 W:  (46) "n" or "Xaa" used, for SEQ ID#:12
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VERIFICATION SUMMARY
PATENT APPLICATION: US/09/972,546

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